

WHAT IS CLAIMED IS:

1. A cultivated, fertile transgenic hybrid maize plant, the genome of which has been augmented through the introduction of a genetic component, preparable by a process that includes the steps of:
 - 5 (a) preparing a DNA composition *in vitro*, which composition includes the genetic component one desires to introduce into the genome of a maize plant;
 - 10 (b) contacting recipient maize cells with said DNA composition under conditions allowing the uptake of the genetic component by recipient cells, said conditions including microprojectile bombardment;
 - 15 (c) regenerating maize plants from recipient cells which have received the genetic component; and
 - 20 (d) identifying a fertile, transgenic maize plant whose genome has been augmented relative to that of the corresponding nontransgenic recipient cells through the stable introduction of said genetic component.

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2. Cells obtained from the plant of claim 1.
- 25
3. Progeny of the plant of claim 1.
- 30 4. Seeds obtained from the plant of claim 3.

5. The transgenic maize plant of claim 1, wherein the genetic component comprises plasmids.

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6. The transgenic maize plant of claim 1, wherein the genetic component comprises a transposable element.

10 7. The transgenic maize plant of claim 6, wherein the transposable element comprises an Ac, Ds or Mu element.

15 8. The transgenic maize plant of claim 1, wherein the genetic component comprises an MAR region.

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9. The transgenic maize plant of claim 1, wherein the genetic component comprises an exogenous gene encoding a selected trait.

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10. The transgenic maize plant of claim 9, wherein the genetic component comprises a promoter and 3' region operatively linked to said exogenous gene.

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11. The transgenic maize plant of claim 10, wherein said promoter comprises a CaMV 35S, CaMV 19S, *nos*, *Adh*, sucrose synthase, R-allele or root cell promoter.

30 12. The transgenic maize plant of claim 9, wherein the recipient cells are

cotransformed with more than one exogenous gene.

13. The transgenic maize plant of claim 12, wherein at least two exogenous genes are positioned on the same DNA segment, and recipient cells are contacted with said segment.
14. The transgenic maize plant of claim 9, wherein the exogenous gene comprises a selectable or screenable marker gene.
15. The transgenic maize plant of claim 14, wherein the selectable or screenable marker gene comprises a *neo* gene, a GUS gene, a *bar* gene, a mutant EPSP synthase (*aroA*) gene, a nitrilase gene, an acetolactate synthase gene, a gene from the R complex, a β -lactamase gene, a luciferase gene, an *xy/E* gene, an α -amylase gene, a methotrexate resistant DHFR gene, a galactosidase gene or a tyrosinase gene.
- 20 16. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a *neo* gene.
- 25 17. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a GUS gene.
- 30 18. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a mutant EPSP synthase gene.

19. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a nitrilase gene.

5 20. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a gene from the R complex.

10 21. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a β -lactamase gene.

15 22. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a acetolactate synthase gene.

20 23. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a luciferase gene.

25 24. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a *xylE* gene.

30 25. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises an α -amylase gene.

26. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a tyrosinase gene.

27. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a methotrexate resistant DHFR gene.

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28. The transgenic maize plant of claim 15, wherein the selectable or screenable marker gene comprises a galactosidase gene.

10 29. The transgenic maize plant of claim 9, wherein the exogenous gene comprises a herbicide resistance gene, an insect resistance gene, an antifreeze protein gene, or an antifungal gene.

15 30. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a glyphosate tolerant EPSP synthase gene.

20 31. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a *Bacillus thuringiensis* toxin gene.

25 32. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a lectin gene.

30 33. The transgenic maize plant of claim 32, wherein the exogenous gene comprises a wheat germ agglutinin gene.

34. The transgenic maize plant of claim 32, wherein the exogenous gene comprises a barley lectin gene.

5 35. The transgenic maize plant of claim 32, wherein the exogenous gene comprises a rice lectin gene.

10 36. The transgenic maize plant of claim 32, wherein the exogenous gene comprises a stinging nettle lectin gene.

15 37. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a hevein gene.

38. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a chitinase gene.

20 39. The transgenic maize plant of claim 29, wherein the exogenous gene comprises an avermectin gene.

25 40. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a cow pea trypsin inhibitor gene.

30 41. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a juvenile hormone esterase gene.

42. The transgenic maize plant of claim 29, wherein the exogenous gene comprises a protease inhibitor gene.

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43. The transgenic maize plant of claim 1, wherein the genetic component comprises DNA not of maize origin.

10 44. A fertile, transgenic hybrid *Zea mays* plant, the genome of which has been augmented by chromosomally integrated DNA which encodes one or more preselected proteins, RNA transcripts or mixtures thereof, wherein said DNA is expressed so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed *Zea mays* plant which does not comprise said
15 DNA, and wherein said DNA is transmittable through normal sexual reproduction of the transgenic maize plant to a subsequent generation plant.

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20 45. The transgenic maize plant of claim 44, wherein said DNA segment comprises an exogenous gene encoding a protein which confers a selected trait.

25 46. The transgenic maize plant of claim 45, wherein said DNA segment comprises a promoter operatively linked to said exogenous gene.

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E1 Sub 47. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a selectable or screenable marker gene comprising a dalapon dehalogenase (*deh*) gene, an anthranilate synthase gene that
30 confers resistance to 5 methyl tryptophan, an aequorin gene, or a gene encoding a cell

wall protein modified to include a unique epitope not normally expressed in maize plants, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of
5 the transgenic maize plant to subsequent generation plants.

48. The transgenic maize plant of claim 47, wherein the gene is positioned on a vector capable of autonomous replication in maize cells.

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49. The transgenic maize plant of claim 48, wherein the gene is positioned in a wheat dwarf virus (WDV) shuttle vector.

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50. The transgenic maize plant of claim 48, wherein the autonomous replication vector comprises a transposable element.

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51. The transgenic maize plant of claim 47, wherein the gene is positioned under the control of a promoter region comprising multiple copies of the 16 bp *ocs* enhancer element.

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52. The transgenic maize plant of claim 47, wherein the selectable or screenable marker gene comprises non-expressed DNA.

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53. The transgenic maize plant of claim 47, wherein the selectable or screenable marker gene comprises a dalapon dehalogenase (*deh*) gene.

~~54. The transgenic maize plant of claim 47, wherein the selectable or screenable marker gene comprises an anthranilate synthase gene that confers resistance to 5 methyl tryptophan.~~

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~~55. The transgenic maize plant of claim 47, wherein the selectable or screenable marker gene comprises an aequorin gene.~~

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56. The transgenic maize plant of claim 47, wherein the selectable or screenable marker gene comprises a gene encoding a cell wall protein modified to include a unique epitope not normally expressed in maize plants.

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57. The transgenic maize plant of claim 56, wherein the selectable or screenable marker gene comprises a gene encoding a antigenically modified HPRG.

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58. The transgenic maize plant of claim 47, wherein the coding sequence of the gene is modified to improve expression in maize.

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59. The transgenic maize plant of claim 58, wherein the modified gene comprises a modified Bt toxin *CryIA(c)* or *CryIA(b)* genes.

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60. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a negatively-selectable marker comprising a cytosine deaminase gene, a T-DNA gene 2, an antisense *bar* gene or an antisense *nptII*

gene, so that the transgenic plant exhibits one or more characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said marker, and wherein said marker is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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61. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising an exogenous gene encoding a selected trait, the gene positioned under the control of an inducible or tissue-specific promoter or enhancer comprising an α -tubulin promoter, an actin promoter, a *rbcS* promoter, an *ocs* promoter, a *nos* promoter, a zein storage protein gene promoter, an ABA-inducible promoter, a turgor-inducible promoter, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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62. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a herbicide resistance trait comprising a *bxn* gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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63. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding an insect resistance trait comprising an oryzacystatin gene, a wheat or barley amylase inhibitor gene, a lipoxygenase gene, an ecdysteroid UDP-glucosyl transferase gene or a DIMBOA synthetic

gene of the *bx* locus, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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64. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a disease resistance trait comprising a cecropin gene, a magainin gene or a pathogenesis related (PR) protein gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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65. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a stress resistance trait comprising a glycerol-3-phosphate acetyltransferase gene, a superoxide dismutase gene or a glutathione reductase gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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66. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a drought resistance trait comprising a mannitol-1-phosphate dehydrogenase gene, a trehalose-6-phosphate synthase gene, a myoinositol O-methyltransferase gene or a Late Embryogenic Protein (LEA) gene, so that the transgenic plant exhibits one or more phenotypic characteristics

that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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- 5 67. A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a grain composition trait comprising an aspartokinase gene, an acetyl-CoA carboxylase gene, an ACP-acyltransferase gene, a β -ketoacyl-ACP synthase gene, an acyl carrier protein gene, a fatty acid desaturase gene, a fatty acid epoxidase gene, a fatty acid hydratase gene, a fatty acid dehydratase gene, a sense or antisense phytoene synthase gene, a sense or antisense phytoene desaturase gene, a sense or antisense lycopene synthase gene, a phytase gene, an ADP-glucose pyrophosphorylase gene, a starch synthase gene, a starch branching enzyme gene or a sucrose synthase gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding
- 10 untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

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